

1 CCAACTGCAC CTCGGTCTTA TCGATTGAAT TCCCCGGGGA TCCTCTAGAG ATCCCTCGAC
61 CTGACCCAC GCGTCCGGAA CCTTTCACAG CCGACAAACT ACGGGGACGA TTTCTGATTO
121 ATTTTTCGCG CTTTCGATCC ACCCTCCTCC CTTCTCATGG GACTTTGGGG ACAAAGCGTC
1 M G L W G O S V
181 CCGACCCGCT CCGACGCTCG AGCAGGGGCG TATCCAGGAG CCGAGGACAG CTCGGGAACC
9 P T A S S A R A G R Y P G A R T A S G T
241 AGACCATGCG TCCTGGACCC CAAGATCCTT AAGTTCGTCG TCTTCATCCT CCGGTTCTCG
29 R P N L L D P K I L K F V V F I V A V L
301 CTGCGGCTCG GGGTGAAGTC TGCCACCATC CCGCGGACAG ACAGAGTTCG CCAGCAGACA
49 L P V R V D E A T I P R Q D E V P Q Q T
361 GTGCGCCAC AGCAACAGAG GCGACGCTC AAGGAGGAG AGTGTCCAGC AGGATCTCAT
69 V A P Q Q Q R R S L K E E E C P A G S H
421 AGATCAGAT ATACTGAGC CTGTAAACCG TGCACAGAG OTGTGGATTA CACCATCTCT
89 R S E Y T G A C N P C T E G V D Y T I A
481 TCCACAAAT TGCCTCTTG CCTGCTATGT ACAGTTTGT AATCAGGTCA AACAAATAA
109 S M N L P S C L L C T V C K S G Q T H K
541 AGTTCCTGTA CCAGACCCAG AGACACCGTG TGTCACTGTG AAAAAGGAG CTTCCAGGAT
129 S S C T T T R D T V C Q C E K G S F Q D
601 AAAAAGTCCC CTGAGATGTG CCGACGCTGT AGACAGGGT GTCCGAGAGG GATGTCAGG
149 K H S P E M C R T C R T C P R G M V K
661 GTCACTAAT GTACGCCCCG GAGTGACATC AAGTCAAAA ATGAATCAGC TCCAGTTC
169 V S H C T P R S D I K C K N E S A A S S
721 ACTGGGAAAA CCCCAGCAGC GAGGAGGACA GTGACACCA TCCTGGGAT GCTTGCCTCT
189 T G K T F A A E E T V T T I L G M L A S
781 CCTATCATC ACCTATCAT CATAGTGGT TTAGTATCA TTTAGCTGT GGTGTGGT
209 P Y H Y L I I I V V L V I I L A V V V V
841 GCTTTTCAT GTCGAAGAA ATTCATTCT TACCTCAAG GCATCTGTC AAGTGTGGA
229 Q F S C R K K F I S Y L K O I C S G G G
901 GAGGTCCCG AAGCTGTGCA CAGAGTCTT TTCCGGGCG GTTCATGTCC TTCACAGTT
249 G G P E R V H R V L F R R R S C P S R V
961 CCGGGGCGC AGGACATGC CCGAACCGG ACCTGAGTA ACAGATATT GCGACCCACC
269 P G A E D N A R N E T L S M R Y L Q P T
1021 CAGGTCTCTG AGCAGGAAT CCAAGGTGAG GAGCTGCGAG AGCTAACCG TGTGACTGTA
289 Q V S E Q E I Q G Q E L A E L T G V T V
1081 GAGT/GCCAG AGGAGCCACA GGTCTCTGTA GACAGGACAG AAGCTGAAG OTGTGAGAG
309 E X₂₄ P E F Q R L L E Q A E A E G C Q R
1141 AGGAGGCTCG TGGTCCAGT GATGACGCT GACTCGGCTG ACATCAGCAC CTTGCTGAT
329 R R L L V P V N D A D S A D I S T L L D
1201 GCTCGGCAA CACTGGAAGA AGGACATGCA AAGGAACAA TTCAGACCA ACTGTTGGC
349 A S A T L E E G H A K E T I Q D Q L V G
1261 TCCGAAAGC TCTTTATGA AGAGATGAG GCAAGCTCTG CTACGCTCG CTTGTGAAG
369 S E K L F Y E E D E A G S A T S C L
1321 AATCTCTCA GGAACCCAGA GCTTCCCTCA TTTACCTTTT CTCTACAAA GCGAGCAGC
1381 CTGAGAGAAA CAGTCCAGTA CTTGACCCAT GCGCCACAA ACTCTACTAT CCAATATGG
1441 GCACTTACC AATGTCCTA GAACTTTGT AACGCACTG GAGTAATTT TATGAATAC
1501 TCGGTGTGAT AAGCAACCG GAGAAATTA TATCAGATC TTGCTGCTAT AGTTATACGA
1561 TTGTGTATTA AGGTCGTTT TAGGCCCAT GCGGTGCTC ATGCTGTAA TCCAGCACT
1621 TTGATAGCT GAGCAGGTO GATTGCTGA GCTCGGAGT TTGAGACCA CTTATCAAC
1681 ACAGTGAAC TCCATCTCAA TTTAAAAAGA AAAAAGTGG TTTAGGATG TCATTCTTG
1741 CAGTCTTCA TCATGAGACA AGTCTTTTT TCTGCTCTT ATATTGCAAG CTCATCTCT
1801 ACTGTTGTTG GCATTTAATG ACATCTAAT ACAGATGCG CACAGCCACA ATGCTTTGCG
1861 TTATGTTTT TTAATTTAG AACGGGATTA TCTGTGATT ACCTGTATT TCAGTTTGG
1921 ATATTTTTGA CTTATGATG AGATTATCA GACGTACCC TATGCTAAG CATGAGATA
1981 TGACTTACG AGGTTGCGC TTAGAGTTT GAGCTTAAAG ATAGATTAT TGGGGCTTA
2041 CCCCCACCTT AATTAGAAGA AACATTTTAT ATTGCTTTAC TA

Fig. 1A

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RTD 1 --MGLWGQSVPTASSARA--GRYPGARTASGTRPWLLDPKILKFVVFIVA
DR4 51 GRGALPTSMGQHGPSARARAGRAPGPRPAREASPRLRVHKTFKFV--VVG
DR5 1 --MEQRGQNAPAASGARKRHG--PGPREARGARGLRVPKTLVLV--VVA
DcR1 1 -----MARIPKTLKFVVVIVA

RTD 47 VLLPVRVDSATIPRQDEVPOQTVAPOQQRSLKEEECPAGSHRSEYTGAC
DR4 99 VLLQVVPSSAATIKLH---DQSIGTQQWEHSPLGELCPPGSHRSEYTGAC
DR5 45 VLLLVSALITQODLAPQORAAPQQRSSPSEGLCPPGHHISEDGRDC
DcR1 17 VLLPVLAYSATTARQEEVPOQTVAPOQQRHSFKGEECPAGSHRSEHTGAC

CRD1

RTD 97 NPCTEGVDYTIASNNLPSCLLCTVCKSGQTNKSSCTTTRDTVCQCEKGSF
DR4 146 NRCTEGVGTYTNASNNLFACLPCTACKSDEEERSPCTTTRNTACQCKPGTF
DR5 95 ISCKYQDYSTHWNLLFCLRCTRCDSGEVELSPCTTTRNTVCQCEEGTF
DcR1 67 NPCTEGVDYTNASNNPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEG

CRD2

RTD 147 QDKNSPEHCRTCRGTGCPRGHVKVSNCPTPRSDIKCKNESAASSTGKTPAAE
DR4 196 RNDNSAEHCRKCSTGCPRGHVKVKDCTPWSIDIECVHKESGNHNIW----
DR5 145 REEDSPEHCRKCRGTGCPRGHVKVGDCPTPWSIDIECVHKESGIIIGVTVAA-
DcR1 117 RNENSPEHCRKCSR-CPSGEVQVSNCPSWDDIQCVVEEFGANAT-----

Fig. 1B

RTD 233 RKKFISYLGKICSGGGGGPERVHRVLFRRRSCPSRVPGAEDNARNETLSN
DR4 269 -GGDPKCMDRVCFWRLG-----LLRGPGAEDNAHNEILSN
DR5 209 --KVLPLYLGKICSGGGGDPERVDR-----SSQRPGAEDNVLNEIVSI

RTD 283 RYLQPTQVSEQEIQGQELAEITGVTVESPEEPQRLLEQAEAEGCQRRRL
DR4 303 ADSLSTFVSEQQMESQEPADLTGVTQSPGEAQCLLGPAEAEGSQRRRL
DR5 250 --LQPTQVPEQEMEVEQEPAEPTGVNMLSPGESEHLLLEPAEAERSQRRRL

RTD 333 VPVNDAD-----DD-----
DR4 353 VPANGADPTETLMLFFDKFANIVPFDSWDQLMRQLDLTKNEIDVVRAGTA
DR5 298 VPANEGDPTETLRQCFDDFADLVPFDSWEPLMRKLGLMDNEIKVAKAEAA

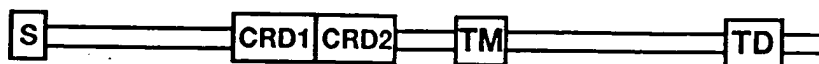
RTD 340 -----SADISTLLDASATLEEGMAKETIQDQLVGSE
DR4 403 GPGDALYAMLKWNKTGRNASIMTLLDALERMEERMAKEKIQDLLVDSG
DR5 348 GHRDTLYTMLIKWNKTGRDASVMTLLDALETGERLAKQKIEDHLLSSG

RTD 371 KLFYEDEAGSATSCL
DR4 453 KFIYLEDGTGSAVSLE
DR5 398 KFMYLEGNADSALS

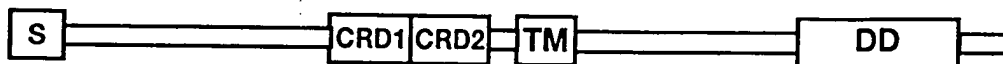
Fig. 1C

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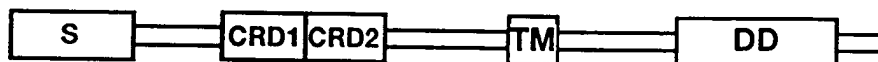
RTD



DR4



DR5



DcR1



Fig. 1D

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06913374.082627 469230-4687580

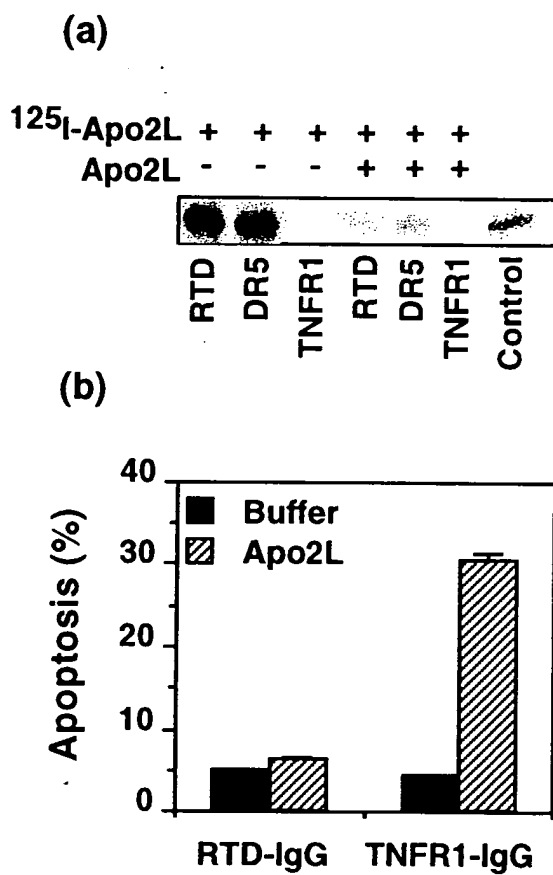


Fig. 2

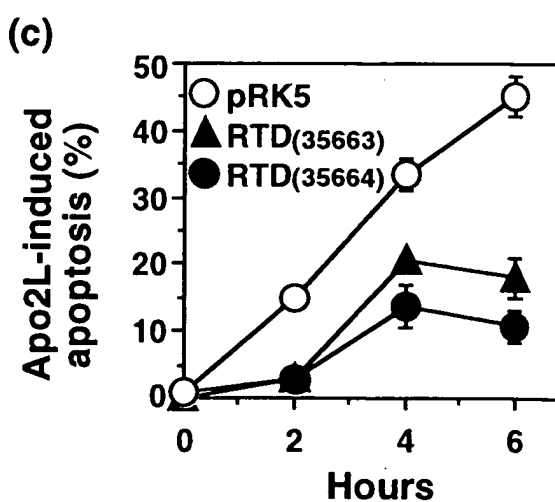
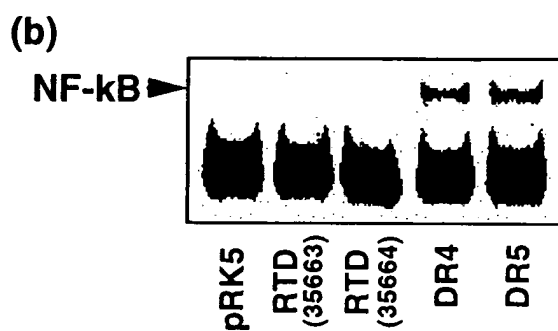
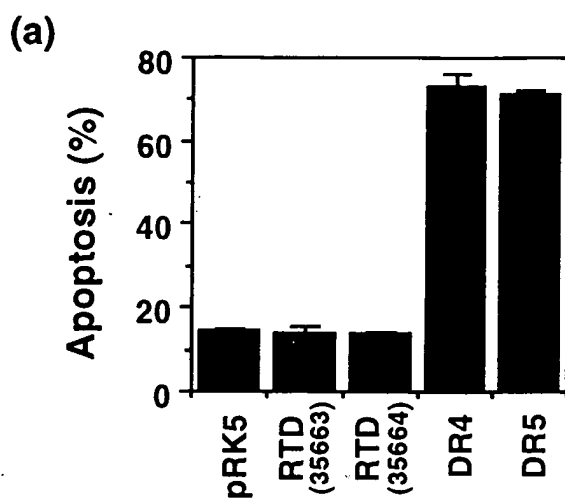


Fig. 3

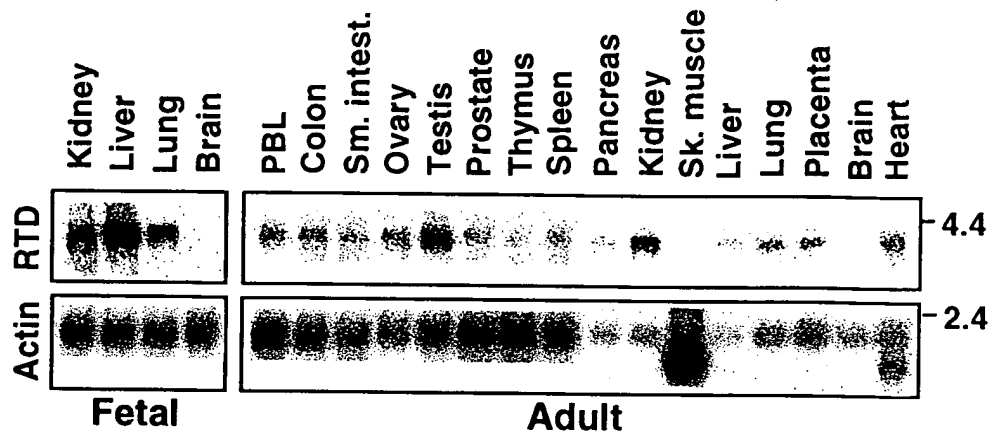


Fig. 4